

BLASTP 2.2.20+

Reference: Stephen F. Altschul, Thomas L. Madden, Alejandro A. Schaffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: YSWSR5KT01R

Database: All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects
 8,267,994 sequences; 2,848,338,404 total letters

Query=

Length=16

Sequences producing significant alignments:	Score (Bits)	E Value
gb AAA30830.1 apolipoprotein C-III precursor	25.2	0.078
gb AAA31389.1 macrophage cationic peptide 2 (MCP-2) >gb AAA3...	21.8	0.82
gb AAA40730.1 amylin precursor >gb AAA41359.1 islet amyloid...	21.8	0.82
gb AAA37874.1 islet amyloid polypeptide	21.8	0.82
gb AAA51760.1 apolipoprotein C-III precursor >gb AAA51761.1 ...	21.8	0.82
gb AAA31387.1 macrophage cationic peptide 1 (MCP-1) precursor...	21.8	0.82
gb AAA30759.1 seminalplasmin precursor	21.4	1.1
gb AAA26479.1 xis-like gene; putative	21.0	1.5
gb AAA18561.1 putative. similar to phospholipid transfer pro...	21.0	1.5
gb AAA31236.1 defensin NP-3a >gb AAA31237.1 defensin NP-3a	20.6	2.0

ALIGNMENTS

>gb|AAA30830.1| apolipoprotein C-III precursor
 Length=100

Score = 25.2 bits (52), Expect = 0.078
 Identities = 9/11 (81%), Positives = 9/11 (81%), Gaps = 0/11 (0%)

Query 5 LLPAVLLALLA 15
 LL A LLALLA
 Sbjct 6 LLVAALLALLA 16

>gb|AAA31389.1| macrophage cationic peptide 2 (MCP-2)
 gb|AAA31390.1| macrophage cationic peptide 2 (MCP-2) precursor
 gb|AAA31424.1| corticostatin CS-4
 Length=95

Score = 21.8 bits (44), Expect = 0.82
 Identities = 9/13 (69%), Positives = 10/13 (76%), Gaps = 1/13 (7%)

Query 4 ALLPAVLL-ALLA 15
 ALL A+LL AL A
 Sbjct 5 ALLAAILLVALQA 17

Score = 17.2 bits (33), Expect = 21
 Identities = 5/5 (100%), Positives = 5/5 (100%), Gaps = 0/5 (0%)

Query 11 LALLA 15
 LALLA
 Sbjct 4 LALLA 8

>gb|AAA40730.1| amylin precursor
 gb|AAA41359.1| islet amyloid polypeptide
 Length=93

Score = 21.8 bits (44), Expect = 0.82
 Identities = 7/8 (87%), Positives = 7/8 (87%), Gaps = 0/8 (0%)

Query 6 LPAVLLAL 13
 LPAVLL L
 Sbjct 7 LPAVLLIL 14

>gb|AAA37874.1| islet amyloid polypeptide
 Length=93

Score = 21.8 bits (44), Expect = 0.82
 Identities = 7/8 (87%), Positives = 7/8 (87%), Gaps = 0/8 (0%)

Query 6 LPAVLLAL 13
 LPAVLL L
 Sbjct 7 LPAVLLIL 14

Score = 9.1 bits (14), Expect = 5560
 Identities = 2/2 (100%), Positives = 2/2 (100%), Gaps = 0/2 (0%)

Query 13 LL 14
 LL
 Sbjct 91 LL 92

>gb|AAA51760.1| apolipoprotein C-III precursor
 gb|AAA51761.1| apolipoprotein C-III precursor
 Length=99

Score = 21.8 bits (44), Expect = 0.82
 Identities = 8/11 (72%), Positives = 8/11 (72%), Gaps = 0/11 (0%)

Query 5 LLPAVLLALLA 15
 LL LLALLA
 Sbjct 6 LLVVALLALLA 16

>gb|AAA31387.1| macrophage cationic peptide 1 (MCP-1) precursor
 gb|AAA31388.1| macrophage cationic peptide (MCP-1)
 Length=95

Score = 21.8 bits (44), Expect = 0.82
 Identities = 9/13 (69%), Positives = 10/13 (76%), Gaps = 1/13 (7%)

Query 4 ALLPAVLL-ALLA 15
 ALL A+LL AL A
 Sbjct 5 ALLAAILLVALQA 17

Score = 17.2 bits (33), Expect = 21
 Identities = 5/5 (100%), Positives = 5/5 (100%), Gaps = 0/5 (0%)

Query 11 LALLA 15
 LALLA
 Sbjct 4 LALLA 8

>gb|AAA30759.1| seminalplasmin precursor
 Length=80

Score = 21.4 bits (43), Expect = 1.1
 Identities = 8/11 (72%), Positives = 8/11 (72%), Gaps = 3/11 (27%)

Query 7 PA---VLLALL 14
 PA VLLALL
 Sbjct 9 PAMATVLLALL 19

>gb|AAA26479.1| xis-like gene; putative
 Length=92

Score = 21.0 bits (42), Expect = 1.5
 Identities = 10/21 (47%), Positives = 13/21 (61%), Gaps = 6/21 (28%)

Query 1 AAVALL-----PAVLLALLA 15
 AAVA+L P +L+A LA
 Sbjct 23 AAVAVLLWRAVLPVILIAALA 43

Score = 20.2 bits (40), Expect = 2.7
 Identities = 9/15 (60%), Positives = 10/15 (66%), Gaps = 4/15 (26%)

Query 1 AAVALLPA----VLL 11
 AA+ALL A VLL
 Sbjct 15 AALALLTAAAVAVLL 29

Score = 18.5 bits (36), Expect = 8.6
 Identities = 7/9 (77%), Positives = 7/9 (77%), Gaps = 2/9 (22%)

Query 8 AVL--LALL 14
 AVL LALL
 Sbjct 12 AVLAALALL 20

Score = 15.9 bits (30), Expect = 50
 Identities = 7/13 (53%), Positives = 10/13 (76%), Gaps = 0/13 (0%)

Query 1 AAVALLPAVLLAL 13
 AA+A L ++LAL
 Sbjct 58 AALAALRGMLAL 70

Score = 13.4 bits (24), Expect = 294
 Identities = 4/5 (80%), Positives = 5/5 (100%), Gaps = 0/5 (0%)

Query 11 LALLA 15
 LA+LA

Sbjct 11 LAVLA 15

Score = 12.9 bits (23), Expect = 394
 Identities = 6/9 (66%), Positives = 6/9 (66%), Gaps = 2/9 (22%)

Query 9 VL--LALLA 15
 VL LA LA

Sbjct 10 VLA VLA ALA 18

>gb|AAA18561.1| putative. similar to phospholipid transfer proteins
 Length=29

Score = 21.0 bits (42), Expect = 1.5
 Identities = 9/14 (64%), Positives = 11/14 (78%), Gaps = 2/14 (14%)

Query 2 AVALLPAVLLALLA 15
 AVA++ AVL LLA
 Sbjct 9 AVAVVAAVL--LLA 20

>gb|AAA31236.1| defensin NP-3a
 >gb|AAA31237.1| defensin NP-3a
 Length=93

Score = 20.6 bits (41), Expect = 2.0
 Identities = 7/10 (70%), Positives = 8/10 (80%), Gaps = 0/10 (0%)

Query 5 LLPAVLLALL 14
 LL A+LLA L
 Sbjct 6 LLAAILLAL 15

Database: All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF
 excluding environmental samples from WGS projects

Posted date: Apr 17, 2009 6:11 PM

Number of letters in database: 306,907

Number of sequences in database: 5,031

Lambda K H
 0.335 0.297 1.50

Gapped

Lambda K H
 0.294 0.110 0.610

Matrix: PAM30

Gap Penalties: Existence: 9, Extension: 1

Number of Sequences: 5031

Number of Hits to DB: 1635

Number of extensions: 77

Number of successful extensions: 77

Number of sequences better than 200000: 49

Number of HSP's better than 200000 without gapping: 0

Number of HSP's gapped: 68

Number of HSP's successfully gapped: 66

Length of query: 16

Length of database: 306907

Length adjustment: 5

Effective length of query: 11

Effective length of database: 281752
Effective search space: 3099272
Effective search space used: 3099272
T: 11
A: 40
X1: 2 (1.0 bits)
X2: 35 (14.8 bits)
X3: 58 (24.6 bits)
S1: 2 (4.0 bits)
S2: 2 (4.0 bits)